

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 1, 2003, 17:48:35 ; Search time 42 Seconds

(without alignments)
929,299 Million cell updates/sec

Title: US-09-782-587b-1

Perfect score: 2187
Sequence: 1 ANAFLXXLRPGSLXKRCXX.....LQKLRSEPPGVLLRAPPP 406

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2167	99.1	466	1 KFH07	coagulation factor
2	1601	73.2	443	2 146932	coagulation factor
3	1566	71.6	407	1 KFB07	coagulation factor
4	858.5	39.3	475	1 EXCH	coagulation factor
5	858.5	39.3	488	1 EXHU	coagulation factor
6	850.5	38.9	416	1 KFB0	coagulation factor
7	849	38.8	461	1 KFHU	coagulation factor
8	843	38.5	492	1 EXBO	coagulation factor
9	831.5	38.0	482	1 EXRT	coagulation factor
10	824	37.7	459	2 J00419	coagulation factor
11	824	37.5	452	1 A30351	coagulation factor
12	781	37.5	159	2 184615	coagulation factor
13	775	35.4	461	1 S18994	coagulation factor
14	769	35.2	461	1 JX0210	coagulation factor
15	749	34.2	456	1 KXBO	coagulation factor
16	726	33.2	461	1 KXHU	coagulation factor
17	519.5	23.8	275	2 146712	coagulation factor
18	515.5	23.6	282	2 184621	coagulation factor
19	513.5	23.5	271	2 146580	coagulation factor
20	511	23.4	285	2 148144	coagulation factor
21	509.5	23.3	274	2 147078	coagulation factor
22	473	21.6	638	1 K0KSP	coagulation factor
23	461.5	21.1	638	1 K0KTP	coagulation factor
24	459.5	21.0	638	1 K0HUP	coagulation factor
25	445.5	20.4	343	1 A57014	coagulation factor
26	444	20.3	625	1 KFHU1	coagulation factor
27	443.5	20.3	622	1 TBHU	coagulation factor
28	439.5	20.1	655	1 A46688	coagulation factor
29	428.5	19.6	625	1 TBBO	coagulation factor

30	428	19.6	1035	1 A43090	enteropeptidase (E
31	426.5	19.5	246	1 TRRT1	trypsin (EC 3.4.21
32	425.5	19.5	618	2 A35827	thrombin (EC 3.4.2
33	423	19.3	229	1 TRDES	trypsin (EC 3.4.21
34	423	19.3	358	2 JC5878	plasma hyaluronan-
35	421	19.3	617	2 S10511	thrombin (EC 3.4.2
36	420.5	19.2	247	2 A27547	trypsin (EC 3.4.21
37	418	19.1	1019	1 A56318	enteropeptidase (E
38	417	19.1	786	1 A47547	serine proteinase
39	417	19.1	1034	1 A53663	enteropeptidase (E
40	416.5	19.0	246	1 TRRT2	trypsin (EC 3.4.21
41	415.5	19.0	855	2 JC7731	membrane-bound arg
42	415.5	19.0	855	2 JC7775	membrane type-1
43	413	18.9	417	1 S00845	hepsin (EC 3.4.21
44	412.5	18.9	248	2 S55066	trypsin (EC 3.4.21
45	411	18.8	810	2 146260	plasmin (EC 3.4.21

ALIGNMENTS

RESULT 1
KFB07
coagulation factor VIIA (EC 3.4.21.21) precursor [validated] - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1989 #sequence, revision 19-May-1994 #text, change 08-Dec-2000
C:Accession: A28322; A23819; A31186; B31186; S63524
R:O'Hara, P.J.; Grant, F.J.; Haldeman, B.A.; Gray, C.L.; Insley, M.Y.; Hagen, F.S.; M
Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987
A:Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-dep
A:Reference number: A28322; MUID:87260948; PMID:3037537
A:Accession: A28322
A:Molecule type: DNA
A:Residues: 1-466 <OH>
A:Cross-references: GB:J02933; NID:9180333; PIDN:AA51983.1; PID:9180334
R:Hagen, F.S.; Gray, C.L.; O'Hara, P.J.; Grant, F.J.; Saari, G.C.; Woodbury, R.G.; Hart
Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986
A:Title: Characterization of a cDNA coding for human factor VII.
A:Reference number: A23819; MUID:86205965; PMID:3486420
A:Accession: A23819
A:Molecule type: mRNA
A:Residues: 1-466 <HAG>
A:Cross-references: GB:M13232; NID:9182799; PIDN:AA88040.1; PID:9182801
R:Thim, L.; Bjoern, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen,
Biochemistry 27, 7785-7793, 1988
A:Title: Amino acid sequence and posttranslational modifications of human factor VII.
A:Reference number: A90539; MUID:8908153; PMID:3264725
A:Accession: A31186
A:Molecule type: protein
A:Residues: 61-212 <THR>
A:Accession: B31186
A:Molecule type: protein
A:Residues: 213-466 <TH2>
R:Bjoern, S.; Foster, D.C.; Thim, L.; Wlberg, F.C.; Christensen, M.; Komiyama, Y.; Pe
J. Biol. Chem. 266, 11051-11057, 1991
A:Title: Human plasma and recombinant factor VII. Characterization of O-glycosylation
A:Reference number: M40529; MUID:9150411; PMID:1904059
A:Contents: annotation; carbohydrate binding sites
R:Persson, E.; Petersen, L.C.
Eur. J. Biochem. 234, 293-300, 1995
A:Title: Structurally and functionally distinct Ca(2+) binding sites in the gamma-car
A:Reference number: S63524; MUID:96096752; PMID:8529655
A:Accession: S63524
A:Molecule type: protein
A:Residues: 61-65; 99-103; 105-109; 213-217; 308-312 <PER>
C:Genetics:
A:Gene: GDB:F7
A:Cross-references: GDB:119897; OMIM:227500
A:Map position: 13q34-13q34
A:Intons: 22/1; 44/1; 97/3; 106/1; 144/1; 191/1; 227/3; 269/1
C:Function:
A:Description: catalyzes the proteolytic activation of coagulation factor X in the pr
coagulation factor IX in the presence of calcium and tissue factor

A:Accession: A14757
 A:Molecule type: protein
 A:Residues: 1-63, 'T', '65-416 <KAT>
 R:McMullen, B.A.; Fujikawa, K.; Kistiel, W.
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983
 A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coagulation factor IX
 A:Reference number: A20274; PMID:83308813; PMID:6688526
 A:Accession: B20274
 A:Molecule type: protein
 A:Residues: 59-63, 'X', '65-69 <MCM>
 R:Choo, K.H.; Gould, K.G.; Rees, D.J.G.; Brownlee, G.G.
 Nature 299, 178-180, 1982
 A:Title: Molecular cloning of the gene for human anti-haemophilic factor IX
 A:Reference number: 145891; PMID:82272386; PMID:6287289
 A:Accession: 145891
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 52-139 <CHO>
 A:Cross-references: GB:J00007; NID:q163053; PIDN:AAA30520.1; PID:q163054
 R:Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga, J. Biochem. 104, 867-868, 1988
 A:Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coagulation factor IX
 A:Reference number: A44556; PMID:89213999; PMID:3149637
 A:Contents: annotation
 A:Note: structure and location of a carbohydrate covalently bound to Ser C:Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with strict C:Function:
 A:Description: catalyzes the proteolytic activation of coagulation factor X in the presence of Factor Xa
 A:Pathway: blood coagulation intrinsic pathway
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamate
 F:1-16/Product: coagulation factor IXa light chain [status experimental <ALC>
 F:1-45/Domain: Gla domain homology (fragment) <GLA>
 F:51-82/Domain: EGF homology <EG1>
 F:88-124/Domain: EGF homology <EG2>
 F:147-181/Domain: activation peptide #status experimental <APT>
 F:182-416/Product: coagulation factor IXa heavy chain [status experimental <AHC>
 F:182-409/Domain: trypsin homology <TRY>
 F:7,8,15,17,20,21,26,27,30,33,36,40/Modified site: gamma-carboxyglutamic acid (Glu) #str F:18-23,51-62,56-71,73-82,88-99,95-109,111-124,133-299,207-223,337-351,362-390/Dsulfide F:53/Binding site: carboxydrate (Ser) (covalent) #status experimental
 F:64/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F:158,166,173,261/Binding site: carboxydrate (Asn) (covalent) #status experimental
 F:222,270,366/Active site: His, Asp, Ser #status predicted

Query Match 38.9%; Score 850.5; DB 1; Length 416;
 Best Local Similarity 40.2%; Pred. No. 5; 1e-56;
 Matches 167; Conservative 68; Mismatches 129; Indels 51; Gaps 9;

OY 11 GSLRXCKXXGCSFYXARXIFKDAKTKLFWISYSDGDCASSPCQNGSGCKDLOSIC 70
 DB 12 GMLRECKREKESFEAREVETEXTETFEWQYVGDGDCSPCLNGCMCKNDINSYC 71
 OY 71 FCLPFEGRNCTHMDOLICVNEGGCGQYSDHTGTTRSCRCHGEGSLADSVCTPT 130
 DB 72 WQAGFEGRNCEL---DATCSIKNGRCKQFCKRDNDNVVSCDTGYRLAEDQKCEPRA 127
 OY 131 VEYPCGKIPIT--LEKR-----NASKP-----GATYGVK 158
 DB 128 VFFPCGRVSVSHSKKLTAEITFSNTYNSSESAIINDNTQSNQSFDESRVVGDD 187
 OY 159 CPKGCPCMOVLILVNGAOLCGTLINTIIVVSAACFCDKIKMNRNLIAVLGEHLSSEHG 218
 DB 188 AERGGFPMQVLLHGEIAAFCCGSISYENKVVTRAHC---IKRGVKTIVAGENHTKPEP 244
 OY 219 DEOSRVAOVITPSPYVET---NHDIALLRLHQVPLVDHVVPLCLPERTSESLIAPV 276
 DB 245 TEQKRNVIRAIPIYHSYNASINKYSHDIALLEDEPLELSYVPICIADRDY---TNIPS 301
 OY 277 RF--SLVSGMGLLRGATLALMLVNLVPRMTQDCLQOSRKVGDSPNTEVFCAGYSD 334

DB 302 KFGYVSGMGKFFNRRGRSASIILOYLKPLVDRATCLRSTKF-----SIYSHFCAGYHE 356
 OY 335 GSKDCGDSGGPETHYRGHWYLTGIVSGGCGATGHHGVYTRVSOYLEMOK 389
 DB 357 GGRDCGDSGGPETHYRGHWYLTGIVSGGCGATGHHGVYTRVSOYLEMOK 411

RESULT 7
 KFHU
 coagulation factor IXa (EC 3.4.21.22) precursor [validated] - human
 N:Alternate names: antihemophilic factor B; Christmas factor
 C:Species: Homo sapiens (hmn)
 C:Date: 17-Dec-1982 #sequence, revision 30-Jun-1987 #text, change 15-Sep-2000
 C:Accession: A00922; A37570; A30511; A32989; A22673; A21337; A37546; A30623; A60486;
 R:Yoshitake, S.; Schach, B.G.; Foster, D.C.; Davie, E.W.; Kurachi, K.
 Biochemistry 24, 3736-3750, 1985
 A:Title: Nucleotide sequence of the gene for human factor IX (antihemophilic factor B
 A:Reference number: A00922; PMID:86000558; PMID:2994716
 A:Accession: A00922
 A:Molecule type: DNA
 A:Residues: 1-461 <ROS>
 A:Cross-references: GB:K02402; NID:q182612; PIDN:AB59620.1; PID:q182613
 R:Ranson, D.S.; Choo, K.H.; Rees, D.J.G.; Glanville, F.; Gould, K.; Huddleston, J.A.;
 EMBO J. 3, 1053-1060, 1984
 A:Title: The gene structure of human anti-haemophilic factor IX
 A:Reference number: A37570; PMID:84236100; PMID:6329734
 A:Accession: A37570
 A:Molecule type: DNA
 A:Residues: 1-461 <ANS>
 A:Cross-references: GB:K02048
 R:Reitma, P.H.; Bertina, R.M.; Ploos van Amstel, J.K.; Riemens, A.; Briet, E.
 Blood 72, 1074-1076, 1988
 A:Title: The putative factor IX gene promoter in hemophilia B Leyden.
 A:Reference number: A30511; PMID:88327116; PMID:3416065
 A:Accession: A30511
 A:Molecule type: DNA
 A:Residues: 8-24 <REH>
 A:Cross-references: EMBL:X55008; NID:q311288; PIDN:CA838245.2; PID:g4469253
 R:Koebberl, D.D.; Bottema, C.D.K.; Buerstedde, J.M.; Sommer, S.S.
 Am. J. Hum. Genet. 45, 448-457, 1989
 A:Title: Functionally important regions of the factor IX gene have a low rate of poly
 A:Reference number: A32989; PMID:89317152; PMID:2773937
 A:Accession: A32989
 A:Molecule type: DNA
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 30-92 <ROE>
 R:McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Lundblad, R.L.; Roberts, H.R.; Graham, J.B.
 Proc. Natl. Acad. Sci. U.S.A. 82, 2847-2851, 1985
 A:Title: Evidence for a prevalent dimorphism in the activation peptide of human coagu
 A:Reference number: A22673; PMID:85190593; PMID:3857619
 A:Accession: A22673
 A:Molecule type: mRNA
 A:Residues: 1-193, 'T', '195-461 <MCG>
 A:Cross-references: GB:M11309; NID:q180552; PIDN:AAA52023.1; PID:q180553
 A:Note: the authors translated the codon ACA for residue 29 as Tyr
 R:Daye, M.; de la Salle, H.; Schamber, F.; Ballard, A.; Kohl, V.; Flindell, A.; Tolst
 Nucleic Acids Res. 11, 2325-2335, 1983
 A:Title: Isolation of a human anti-haemophilic factor IX cDNA clone using a unique 52
 A:Reference number: A21337; PMID:83220788; PMID:6687940
 A:Accession: A21337
 A:Molecule type: mRNA
 A:Residues: 1-193, 'T', '195-461 <JAV>
 A:Cross-references: GB:J00137; NID:q182610; PIDN:AAA52763.1; PID:q182611
 R:Tagadavaran, P.; Lavelle, D.E.; Kaul, R.; Mohandas, T.; Warren, S.T.
 Somat. Cell Mol. Genet. 10, 465-473, 1984
 A:Title: Isolation and characterization of human factor IX cDNA: identification of Ta
 A:Reference number: A37546; PMID:84300526; PMID:6089357
 A:Accession: A37546
 A:Molecule type: mRNA
 A:Residues: 38-193, 'T', '195-326 <JAG>
 A:Cross-references: GB:M35672
 R:Kurachi, K.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 79, 6461-6464, 1982

A:Title: Isolation and characterization of a cDNA coding for human factor IX.
 A:Reference number: A30623; MUID:83065193; PMID:6959130
 A:Accession: A30623
 A:Molecule type: mRNA
 A:Residues: 1-12, 'S', 14-73, 'P', 75-82, 'K', 84-203, 'P', 205-216, 'G', 218-298, 'A', 299-356, 'A',
 A:Cross-references: GB:J00136; NID:9182608; PIDN:AAA98726.1; PID:9182609
 A:Experimental source: liver
 R:Tharakan, J.; Strickland, D.; Burgess, W.; Drohan, W.N.; Clark, D.B.
 Vox Sang. 58, 21-29, 1990
 A:Title: Development of an immunoaffinity process for factor IX purification.
 A:Reference number: A60486; MUID:90194857; PMID:2316207
 A:Accession: A60486
 A:Molecule type: protein
 A:Residues: 47-52, 'XX', 55-60, 'X', 62, 'XX', 65 <THA>
 R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983
 A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coagulation factors.
 A:Reference number: A20274; MUID:83308813; PMID:6688526
 A:Accession: A20274
 A:Molecule type: protein
 A:Residues: 105-109, 'X', 111-115 <KCM>
 R:Balland, A.; Faure, T.; Carvallo, D.; Cordier, P.; Ulrich, P.; Fournet, B.; de la Salle, J.
 Eur. J. Biochem. 172, 565-572, 1988
 A:Title: Characterisation of two differently processed forms of human recombinant factor IX.
 A:Reference number: S02527; MUID:88166735; PMID:3280312
 A:Accession: S02527
 A:Molecule type: protein
 A:Residues: 29-63 <BAL>
 A:Note: processed forms expressed in recombinant system
 R:Ballat, S.; Perraud, F.; Dalemans, W.; Balland, A.; Dlesterle, A.; Faure, T.; Meullen, EMO J. 9, 3295-3301, 1990
 A:Title: Characterization of recombinant human factor IX expressed in transgenic mice at the embryonic stage.
 A:Reference number: S12058; MUID:91006024; PMID:2209546
 A:Accession: S12058
 A:Molecule type: mRNA; protein
 A:Residues: 1-68 <JAL>
 A:Note: processed forms expressed in recombinant system
 R:Handford, P.A.; Barron, M.; Mayhew, M.; Willis, A.; Beesley, T.; Brownlee, G.G.; Campobasso, EMO J. 9, 475-480, 1990
 A:Title: The first EGF-like domain from human factor IX contains a high-affinity calcium binding site.
 A:Reference number: S12377; MUID:90151623; PMID:2406129
 A:Accession: S12377
 A:Molecule type: protein
 A:Residues: 92-130 <HAN>
 A:Note: NMR detection of calcium binding by domain expressed in recombinant system
 R:de la Salle, C.; Charmanlier, J.L.; Baas, M.J.; Schwartz, A.; Miesel, M.L.; Grunbaum, Thromb. Haemost. 70, 370-371, 1993
 A:Title: A deletion located in the 3' non translated part of the factor IX gene responsible for a severe bleeding disorder.
 A:Reference number: I59612; MUID:94054330; PMID:8236150
 A:Accession: I59612
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 444-461 <RES>
 A:Cross-references: GB:S66752; NID:9439773; PIDN:AA8588.1; PID:9439774
 R:Stoffel, E.S.; Koeberl, D.D.; Sarkar, G.; Sommer, S.S.
 Science 239, 491-494, 1988
 A:Title: Genomic amplification with transcript sequencing.
 A:Reference number: I59529; MUID:88127096; PMID:3340835
 A:Accession: I59529
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 290-359 <RE2>
 A:Cross-references: NID:9182622; PIDN:AAA52456.1; PID:9182623
 R:Agarwal, K.L.; Kawabata, S.; Takao, T.; Murata, H.; Shimonishi, Y.; Nishimura, H.; Iwano, Biochemistry 33, 5167-5171, 1994
 A:Title: Activation peptide of human factor IX has oligosaccharides O-glycosidically linked to the propeptide.
 A:Reference number: A54255; MUID:94227047; PMID:8178292
 A:Accession: A54255
 A:Molecule type: protein
 A:Residues: 'D', 204, 'X', 206-211, 212, 'D', 214, 'X', 216-221, 'D', <AG2>
 A:Note: the residues designated 'X' were determined to be threonine bound to carbohydrate
 R:Di Sciopio, R.G.; Kurachi, K.; Dayle, E.W.
 J. Clin. Invest. 61, 1528-1538, 1978

A:Title: Activation of human factor IX (Christmas factor).
 A:Reference number: A16483; MUID:78194509; PMID:659613
 A:Contents: annotation; activation; active site; carbohydrate binding
 R:McGraw, R.A.; Davy, L.M.; Noyes, C.M.; Graham, J.B.; Roberts, H.R.; Stafford, D.
 Am. Soc. Hematol. Abstr. 64(Suppl.1), 262a, 1984
 A:Reference number: A37569
 A:Contents: annotation
 A:Note: 194-Thr was also found
 R:Morita, T.; Isaacs, B.S.; Esmen, C.T.; Johnson, A.E.
 J. Biol. Chem. 259, 5698-5704, 1984
 A:Title: Derivatives of blood coagulation factor IX contain a high affinity Ca2+-binding site.
 A:Reference number: A37543; MUID:84185715; PMID:6425296
 A:Contents: annotation; calcium binding
 R:Morita, T.; Isaacs, B.S.; Esmen, C.T.; Johnson, A.E.
 J. Biol. Chem. 260, 2583, 1985
 A:Reference number: A37544
 A:Contents: annotation; calcium binding, correction
 R:Bentley, A.K.; Rees, D.J.G.; Rizza, C.; Brownlee, G.G.
 Cell 45, 343-348, 1986
 A:Title: Defective propeptide processing of blood clotting factor IX caused by mutation at the propeptide processing site.
 A:Reference number: A37545; MUID:86189947; PMID:3009023
 A:Contents: annotation; signal sequence cleavage site
 R:Suethiro, K.; Kawabata, S.I.; Miyata, T.; Takeya, H.; Takamatsu, J.; Ogata, K.; Kari, J. Biol. Chem. 264, 21257-21265, 1989
 A:Title: Blood clotting factor IX (B₉) Nagoya: substitution of arginine 180 by tryptophan.
 A:Reference number: A50622; MUID:90078229; PMID:2593373
 A:Contents: annotation; sequence of mutant (B₉) Nagoya
 A:Note: carboxylation, glycosylation, and cleavage sites
 R:Barron, M.; Norman, D.G.; Harvey, T.S.; Hanford, P.A.; Mayhew, M.; Tse, A.G.D.; Brc submitted to the Brookhaven Protein Data Bank, November 1991
 A:Reference number: A51252; PDB:1IXA
 A:Contents: annotation; conformation by (1)H-NMR, residues 92-130
 A:Note: recombinant form expressed in yeast
 C:Comment: Factor IX is activated by factor XIa, which excises the activation peptide
 C:Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K-dependent, modification
 C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with A:Gene: GDB:F9
 A:Cross-references: GDB:119900; OMIM:306900
 A:Map position: Xq27.1-Xq27.2
 A:Insertions: 30/1; 84/2; 93/1; 131/1; 174/1; 241/3; 280/1
 A:Function:
 A:Description: catalyzes the proteolytic activation of coagulation factor X in the presence of factor V and phospholipids
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylated; signal sequence; status predicted <SIG>
 F:1-28/Domain: signal sequence #status predicted <SIG>
 F:29-46/Domain: propeptide #status experimental <PPT>
 F:31-91/Domain: Gla domain homology <GLA>
 F:47-191/Product: coagulation factor IXa light chain #status experimental <ALC>
 F:97-128/Domain: EGF homology <EGF>
 F:134-170/Domain: EGF homology <EGF>
 F:192-226/Domain: activation peptide #status experimental <ACT>
 F:227-461/Product: coagulation factor IXa heavy chain #status experimental <AHC>
 F:227-461/Domain: trypsin homology <TRY>
 F:53, 54, 61, 63, 66, 67, 72, 73, 76, 79, 82, 86/Modified site: gamma-carboxyglutamic acid (Glu) F:64-69, 97-108, 102-117, 119-128, 134-145, 141-155, 157-170, 178-335, 252-268, 382-396, 407-411/Binding site: carboxylate (Ser) (covalent) #status experimental
 F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F:191-192/Cleavage site: Arg-Ala (coagulation factor IXa) #status experimental
 F:203, 213/Binding site: carboxylate (Asn) (covalent) #status experimental
 F:205, 215/Binding site: carboxylate (Thr) (covalent) #status experimental
 F:226-227/Cleavage site: Arg-Val (coagulation factor IXa) #status experimental

Query Match 38.8%; Score 849; DB 1; Length 461;
 Best local similarity 38.9%; Pred. No. 7; 4e-56;
 Matches 161; Conservative 71; Mismatches 132; Indels 50; Gaps 7;
 QY 11 GSLRXXKXXQCSFXXARXIFKDXRTKFTWYSYSGDCASPCQNGSSCKDQLOSLYIC 70
 DB 58 GNLRECHKEKESFEAREVFERTEFTFMQYVDGDCESPCNLGSKDINDSYIC 117
 QY 71 FLPAFEGRNCEETHKDDQLICVNGGCEQYCSDHGTGRSCRGEGYSLADGVSCPT 130


```

Db      118 MCFPEFEGNCEL-----DYTCNKNGRCQFCKNSADNKNVSCSTGYIALAOKSCFEPA 173
Oy      131 VEYPCGKPILEKRNASKPGQ-----RIVGKVC 159
Db      174 VPFPCGRVSVSOTSLKTRAEAVFPDQVDYNSTEAETILDNITQSFNDPFRVVGEDA 233
Oy      160 PKGCEPMOVLILVNAOJCGGTLINTIYVYSAHCEPDKKNNRLAVIGEEDLSHDD 219
Db      234 KPGCFPMOVLNKGKVDACFGGSGIVNEKMTVTAAHC---VETVKITVAVGEINIEETERT 290
Oy      220 EGSRAVAVIIPSTVYVPGTT--NHDIALLRLHQPVLVTHVYPLCLPETFSERTLAFFR 277
Db      291 EGRKRVVILIPHNHNNALINKNNHIALLEDEPLVNSYVTPICADK---EYTNIFRK 347
Oy      278 F--SLVSGMGLLDGAFALMLVNLPLMTQDCLQOSRKVDSPNTEYMFCAQYSDG 335
Db      348 FGSGYVSGMGRFHFHGRSALVLYQVLRVPLVDRATCLRSYK-----TIVNNKCGAGFHGG 402
Oy      336 SKDSCKSGDGGPHAHYHGTWLTGIVSGGCAATVGHGVYTRVSOYTEMJLCK 389
Db      403 GRDSCQSGDGGPHYHVEGTSTLTGIIISWGECAMKGRGYITKVSRYVNMIRKE 456

```

RESULT 8

EXBO

coagulation factor Xa (EC 3.4.21.6) precursor - bovine

N:Alternate names: Stuart factor

C:Species: Bos primigenius taurus (cattle)

C:Date: 24-Apr-1984 #sequence-revision 17-Mar-1987 #text-change 16-Jul-1999

C:Accession: A22867; A14997; A12030; A34412; S39414; A00925

R:Fung, M.R.; Campbell, R.M.; McGillivray, T.A.

Nucleic Acids Res. 12, 4481-4492, 1984

A:Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing a

A:Reference number: A22867; MUID:84247315; PMID:6330671

A:Accession: A22867

A:Molecule type: mRNA

A:Residues: 1-487 <FUN>

A:Cross-references: GB:X00673; MID:g192; PID:CAA25286.1; PID:g193

R:Enfield, D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titani, K.

Biochem. Biophys. Res. Commun. 115, 8-14, 1983

A:Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).

A:Reference number: A14997; MUID:80130563; PMID:6766735

A:Accession: A14997

A:Molecule type: protein

A:Residues: 41-102, N, 104-180 <ENF>

R:McMullen, B.A.; Fujikawa, K.; Kistiel, W.

Biochem. Biophys. Res. Commun. 115, 8-14, 1983

A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co

A:Reference number: A20274; MUID:83308813; PMID:6688526

R:Titani, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.

Proc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975

A:Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.

A:Reference number: A12030; MUID:76053069; PMID:1059093

A:Accession: A12030

A:Molecule type: protein

A:Residues: 183-232, 294-295, 'GDE', 299-334, 336-348, 'AE', 351-354, 356-441, 'GKFG', 446-492 <T

A>Note: carboxydirect binding sites and disulfide bonds were determined

R:Persson, E.; Selander, M.; Linse, S.; Drakenberg, T.; Oehlén, A.K.; Stenflo, J.

J. Biol. Chem. 264, 16897-16904, 1989

A:Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal

A:Reference number: A34412; MUID:89380326; PMID:2789221

A:Accession: A34412

A:Molecule type: protein

A:Residues: 85-126 <PER>

A>Note: beta-hydroxyaspartic acid site

R:Imoue, K.; Morita, T.

Eur. J. Biochem. 218, 153-163, 1993

A:Title: Identification of O-linked oligosaccharide chains in the activation peptides of

A:Reference number: S39414; MUID:94062825; PMID:8243461

A:Accession: S39414

A:Molecule type: protein

```

A:Residues: 183-196,199-209,216-233 <INO>
A>Note: carbohydrate binding sites
R:Titani, K.; Hermodson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.
Biochemistry 11, 4899-4903, 1972
A:Title: Bovine factor X-1a (activated Stuart factor). Evidence of homology with mam
A:Reference number: A1453; MUID:73053314; PMID:4264286
A:Contents: annotation; active site
Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975
R:Fujikawa, K.; Titani, K.; Davie, E.W.
A:Title: Activation of bovine factor X (Stuart factor): conversion of factor Xalpha
A:Reference number: A13504; MUID:76053121; PMID:1059122
A:Contents: annotation; activation
R:Sugo, T.; Bjork, I.; Holmgren, A.; Stenflo, J.
J. Biol. Chem. 259, 5705-5710, 1984
A:Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxygluta
A:Reference number: A38024; MUID:84185716; PMID:6546930
A:Contents: annotation; calcium binding
R:Morita, T.; Jackson, C.M.
J. Biol. Chem. 261, 4008-4014, 1986
A:Reference number: A38025; MUID:86140210; PMID:3949800
A:Contents: annotation; sulfate binding
C:Comment: Factor Xa converts prothrombin to thrombin during blood clotting.
C:Comment: The two chains are formed from a single-chain precursor by the excision of
C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway)
activation.
C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with s
C:Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vita
A:Gene: F10
A:Map position: 13q34
C:Function:
A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the
A:Pathway: blood coagulation
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglu
F:1-15/Domain: signal sequence #status predicted <PRO>
F:16-40/Domain: propeptide #status predicted <PRO>
F:41-180/Domain: Gla domain homology <GLA>
F:90-121/Domain: EGF homology <EG1>
F:129-164/Domain: EGF homology <EG2>
F:183-492/Product: coagulation factor X heavy chain #status experimental <LCH>
F:183-233/Domain: activation peptide #status experimental <AP>
F:234-492/Product: coagulation factor Xa heavy chain #status experimental <AHG>
F:234-461/Domain: trypsin homology <TRY>
F:46-47, 54, 56, 59, 60, 65, 66, 69, 72, 75, 79/Modified site: gamma-carboxyglutamic acid (Glu)
F:57-62, 90-101, 95-110, 112-121, 129-140, 136-149, 151-164, 172-341/Disulfide bonds: #statu
F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F:208/Binding site: sulfate (Tyr) (covalent) #status experimental
F:208/485/Binding site: carbohydrate (Thr) (covalent) #status experimental
F:218/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:233-234/Cleavage site: Arg-Tile (coagulation factor IXa, coagulation factor VIIa) #s
F:240-245, 260-276, 389-403, 414-442/Disulfide bonds: #status experimental
F:275, 321, 418/Active site: His, Asp, Ser #status predicted

```

Query Match

Best Local Similarity 37.5%; Score 843; DB 1; Length 492;

Matches 165; Conservative 70; Mismatches 147; Indels 56; Gaps 7;

```

Oy      1 ANAFILXLRPGLSLRXKXKXOCFFXXARXIFKDXKRTKLEWISYSDGQACSSPCONGS 60
Db      41 ANSFLVEEYKQGNLRECELEACSLFEAREVEDAEQDFEFSKYKDDQDCGHCNLOGH 100
Oy      61 CKDOLQVIFCCLAFGRNCEHTKDDQLCVNNGGCEQYCSHTGTGKSCRHEYSYL 120
Db      101 CKDGGDTCTCAGDEKNECFSTRE--TCSLDNGGCDQCFRERSEVR--CSCAGHYVL 157
Oy      121 LADGVSCTPYVEYPCGKPILEK----- 144
Db      158 GDDSKSCVSTFRFCGFTQGRSRRAHISDALDASELEHDPADLSPESLDLGL 217
Oy      145 NASRPGQ-----RIVGKRVCPKGCPCMOVLL--VNGAQLCGGTLINTIYVYSAHCF 195

```

Db 218 NRTEPSAGEDSGQVRIYGRDCAEGCPQALLVNEENEGFCGTLINERYVTAACHL 277
 QY 196 DKINMRNLIVLGEHDLSEHDGDSRRVAQVIIPSTYVPGTNNHIALRLHQPVLT 255
 Db 278 HQARF---TVRVDRNRTEDEGENMAHEVEMTKHSRFEVETDFDIALRLKTPTRFR 334
 QY 256 DHVPLCLPRTFERTSLAFVRFSLVSGNGQLDRGATALEMLNLNPRMTODCLQOSR 315
 Db 335 RNVAAPCLPEKQMDATLMOKTGVSGFGTHRGRLSSTLKLTPYVDRSTC----- 389
 QY 316 KVGDSNPITEYMFACAGSDGSKDSCGPHATHRGATWYLTGIVSGGCGATVGHFG 375
 Db 390 KLSSSFITPMFACAGSDTQPEDACOGDSGPHATRKDYVTGELVSGEGCARCKRFG 449
 QY 376 YTVRSQYIEMLOKLMRS 393
 Db 450 YTKVSNFLKWKIDRKIMKA 467

RESULT 9

EXRT

coagulation factor Xa (EC 3.4.21.6) precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 31-Jan-1995 #sequence_revision 07-Feb-1997 #text_change 08-Dec-2000
 C:Accession: S49075; J04670; PS0191; PS0190; 162745
 R:Stanton, C.; Ross, R.P.; Hutson, S.; Wallin, R.
 Thromb. Res. 80, 63-73, 1995
 A:Title: Evidence for competition between vitamin K-dependent clotting factors for intra
 A:Reference number: A58498; MUID:96093366; PMID:8578539
 A:Accession: S49075
 A:Molecule type: mRNA
 A:Residues: 1-482 <STAL>
 A:Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A>Note: submitted to the EMBL Data Library, June 1994
 R:Stanton, C.; Ross, R.P.; Hutson, S.; Wallin, R.
 Gene 169, 269-273, 1996
 A:Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.
 A:Reference number: J04670; MUID:96194815; PMID:8647460
 A:Accession: J04670
 A:Molecule type: mRNA
 A:Residues: 1-482 <STAL>
 A:Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A:Experimental source: Cos-1 cell
 R:Enjyoji, K.; Miyazaki, K.; Kato, H.
 J. Biochem. 109, 890-898, 1991
 A:Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat pla
 A:Accession: PS0191
 A:Molecule type: Protein
 A:Residues: 41-58 'X', 60-65 <ENL1>
 A:Accession: PS0190
 A:Molecule type: Protein
 A:Residues: 183-186 'X', 188-207 <ENJ2>
 R:Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.
 Eur. J. Haematol. 52, 162-166, 1994
 A:Title: Analysis of the partial nucleotide sequences and deduced primary structures of
 A:Reference number: I6196; MUID:94222160; PMID:8168596
 A:Accession: I6196
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 295-383, 'G', 385-455 <MUR>
 A:Cross-references: GB:D21215; NID:9415309; PIDN:BA04756.1; PID:9455396
 C:Function:
 A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr
 A:Pathway: blood coagulation
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutan
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-40/Domain: signal sequence #status predicted <PRO>
 F:25-84/Domain: Gla domain homology <GLA>
 F:41-179/Domain: coagulation factor X light chain #status predicted <LCH>
 F:190-121/Domain: EGF homology <EG1>

F:129-164/Domain: EGF homology <EG2>
 F:183-482/Product: coagulation factor X heavy chain #status predicted <HCH>
 F:183-231/Domain: activation peptide #status predicted <APT>
 F:232-482/Product: coagulation factor Xa heavy chain #status predicted <ACT>
 F:232-482/Domain: trypsin homology <TRY>
 F:46,47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxylglutamic acid (Glu) #
 F:57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-340,238-243,259-275,388-40
 F:187/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
 F:208/Binding site: carboxylate (Asn) (covalent) #status experimental
 F:218/Binding site: carboxylate (Thr) (covalent) #status predicted
 F:231-232/Cleavage site: Arg-116 (coagulation factor IXa, coagulation factor VIIa) #
 F:274,320,417/Active site: His, Asp, Ser #status predicted

Query Match 38.08; Score 831.5; DB 1; Length 482;
 Best Local Similarity 36.1%; Pred. No. 1.6e-54;
 Matches 159; Conservative 83; Mismatches 144; Indels 55; Gaps 7;

QY 1 ANAFLLXLRPGSLRXKCKXKQSEFXARXFKAXTKLFWISYSGDQASSPCONGS 60
 Db 41 ANSFPEIKKGNLERECVEICFSEARREVEENETTERWKNYEDGDCSSPCONGE 100
 QY 61 CNDOLSYICFLPAFEGNCEYHNDQILCVNCGCEQYCSGHTGTRSCCHGYSL 120
 Db 101 CRDGLASYCTCTEGFEGKNCLEFV--RLKLSLNDCCQFCNEQNSV-VSCAKGYFL 157
 QY 121 LADGVSTPTVEPCSKT-----PILEKR 144
 Db 158 GNDGKSCSLTAPFPCCKTKTKRAKRSVALNTSNSEPPDPLMDPADILVPTESPSSLNL 217
 QY 145 NASKPQ-----RIYGVKCPKCECPMOLLVYNAO--LCGGLINTIYVNAHCFD 196
 Db 218 NTEPEANSDVIRIYGGGCEKRGCEPMWALLFSEETGDFGCGTILNEFYILTAHCLH 277
 QY 197 KIKMRNLIVLGEHDLSEHDGDSRRVAQVIIPSTYVPGTNNHIALRLHQPVLTLD 256
 Db 278 QAKRRF---VRVGDLTNEDEGGEVNEVDMLIKHKKFRDYYDIDIALRLKTPTRFR 334
 QY 257 HVPPLCLPRTFERTSLAFVRFSLVSGNGQLDRGATALEMLNLNPRMTODCLQOSR 316
 Db 335 RNVAAPCLPEKQMDATLMOKTGVSGFGTHRGRLSSTLKLTPYVDRSTC-----R 389
 QY 317 VGDSPNITEYMFACAGSDGSKDSCGPHATHRGATWYLTGIVSGGCGATVGHFG 376
 Db 390 LSTSFITPMFACAGSDTQPEDACOGDSGPHATRKDYVTGELVSGEGCARCKRKYGI 449
 QY 377 YTVRSQYIEMLOKLMRSEPR 397
 Db 450 YTKVTAFLKWKIDRSKARVGP 470

RESULT 10

coagulation factor IXa (EC 3.4.21.22) precursor - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 16-Jul-1999
 C:Accession: J00419; I49667
 R:Wu, S.M.; Stafford, D.W.; Ware, J.
 Gene 86, 275-278, 1990
 A:Title: Deduced amino acid sequence of mouse blood-coagulation factor IX.
 A:Reference number: J00419; MUID:90215309; PMID:2323576
 A:Accession: J00419
 A:Molecule type: mRNA
 A:Residues: 1-459 <WUS>
 A:Cross-references: GB:M23109; NID:9193317; PIDN:AAA37629.1; PID:9387158
 A:Experimental source: liver
 R:Sarkar, G.; Koehler, D.D.; Sommer, S.S.
 Genomics 6, 133-143, 1990
 A:Title: Direct sequencing of the activation peptide and the catalytic domain of the
 A:Reference number: I46580; MUID:90152675; PMID:2303254
 A:Accession: I49667
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA


```

Db      1 EHEGDEQSRRAVQVILPSTYVGLATNHDIALRLRQPPVLTIDHVPFLCLPEMSEBRTLA 60
        ||:|||||
Qy      275 FVRFSLVSGWGLDRGATLALVLPRLMTQDCLQOSRVGDSPTITEYMFAGYSD 334
        ||:|||||
Db      61 FVRFSLVSGWGLDRGATLALVLPRLMTQDCLQOSRVGDSPTITEYMFAGYSD 120
        ||:|||||
Qy      335 GSKDSCKDGSGGPHATYRGTYLTGIYSGWGGCAVNGH 373
        ||:|||||
Db      121 GSRDSCKDGSGGPHATYRGTYLTGIYSGWGGCAVNGH 159
        ||:|||||

```

RESULT 13

```

S18994
protein C (activated) (EC 3.4.21.69) precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 29-Oct-1999
C:Accession: S18994; S24312
R:Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.
submitted to the EMBL Data Library, February 1992
A:Description: The cDNA cloning and mRNA expression of rat protein C.
A:Reference number: S18994
A:Accession: S18994
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-461 <OKA>
A:Cross-references: EMBL:X64336; NID:q56962; PIDN:CAA45617.1; PID:q56963
R:Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.
Biochim. Biophys. Acta 1131, 329-332, 1992
A:Title: The cDNA cloning and mRNA expression of rat protein C.
A:Reference number: S24312; MUID:92329550; PMID:1627650
A:Accession: S24312
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-461 <OKA>
A:Cross-references: EMBL:X64336; NID:q56962; PIDN:CAA45617.1; PID:q56963
R:Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.
Biochim. Biophys. Acta 1131, 329-332, 1992
A:Title: The cDNA cloning and mRNA expression of rat protein C.
A:Reference number: S24312; MUID:92329550; PMID:1627650
A:Accession: S24312
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-461 <OKA>
A:Cross-references: EMBL:X64336; NID:q56962; PIDN:CAA45617.1; PID:q56963
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; glycoprotein; hydrolase; serine proteinase
F:1-32/Domain: signal sequence #status predicted <SIG>
F:32-85/Domain: Gla domain homology <GUA>
F:33-42/Domain: propeptide #status predicted <PRO>
F:43-461/Product: protein C #status predicted <PC>
F:91-130/Domain: EGF homology <EG1>
F:139-174/Domain: trypsin homology <EG2>
F:213-445/Domain: EGF homology <EG2>
F:47-48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status
F:112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F:121-130,139-150,146-159,161-174,182-320,239-255,373-387,398-426/Disulfide bonds: #stat
F:215,291,355/Binding site: carboxydrate (Asn) (covalent) #status predicted
F:254,300,402/Active site: His, Asp, Ser #status predicted

```

```

Query Match      35.4%; Score 775; DB 1; Length 461;
Best Local Similarity 37.7%; Pred. No. 2.4e-50;
Matches 164; Conservative 67; Mismatches 156; Indels 48; Gaps 11;

```

```

Qy      1 ANAFLLXLRPGSLKRXCKXKXCSFXAXRIFKDXARTLFWISYSDGQCS----- 52
        ||:|||||
Db      42 ANSFLLEKRPASLEKRECEIEICDFEAEQEIIONVEDTIAFWIKIFKFDGQCCSTPLDHCD 101
        ||:|||||
Qy      53 SPONGSGCKDQLOSYICFLPAFEGRNCEHKKDDQLCVNENGCEQYCDHTGTRKSC 112
        ||:|||||
Db      102 SPCGHGTCIDIGLGGFSQCKGWEGRCCQDEMPQ-DCKRKNGGCVHYCLEETRRGR-C 159
        ||:|||||
Qy      113 RCHGEGSLADGVCSTPVEYPCGKIPLEKRNASKPOG-----RIVGG 156
        ||:|||||
Db      160 RCAGGYELADDDHMKCRPVNPPCKR---LAKRTDKKRNKFRDIDPEDELELGRPIYNG 216
        ||:|||||
Qy      157 KVCPRGECPCVOLLVNGAOL-CGGTLINTIWWVSAACFPKIKMRLIAVLGEHDLSE 215
        ||:|||||
Db      217 TLTKGDSFPAAILDSSKKKLACGGVLHTSWVLTAACLESSR---KLTVRLGEYDLRR 273
        ||:|||||
Qy      216 HDGDSQSRRAVQVILPSTYVGLATNHDIALRLRQPPVLTIDHVPFLCLPEMSEBRTLA 275
        ||:|||||

```

```

Db      274 RDPWELODIREVLVHPNTRNSNDIALLSLSPATLSKTIPTICLPNSGLAELLSOA 333
        ||:|||||
Qy      276 VRFSLVSGWGLD-----RGATLALVLPRLMTQDCLQOSRVGDSPTITEYMF 329
        ||:|||||
Db      334 GQETVTVTGWGVQSDKVKQDGRNRRTFI-LTFIRIPLAARDCAQVNNV-----VSENMIC 387
        ||:|||||
Qy      330 AGVSDGSKDSCGSGGPHATYRGTYLTGIYSGWGGCAVNGHGVYTRVSYQYLEWLOK 389
        ||:|||||
Db      388 AGIIDTRDAGCDGSGGPHATYRGTYLTGIYSGWGGCAVNGHGVYTRVSYQYLEWLOK 447
        ||:|||||
Qy      390 LMRSEPRGVLLRAP 404
        ||:|||||
Db      448 YIGER---DVSLKSP 459
        ||:|||||

```

RESULT 14

```

JX0210
protein C (activated) (EC 3.4.21.69) precursor - mouse
N:Alternate names: vitamin K-dependent serine proteinase
N:Alternate names: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: JX0210
R:Tada, N.; Sato, M.; Tsujimura, A.; Iwase, R.; Hashimoto-Gotoh, T.
J. Biochem. 111, 491-495, 1992
A:Title: Isolation and characterization of a mouse protein C cDNA.
A:Reference number: JX0210; MUID:92316897; PMID:1618739
A:Accession: JX0210
A:Molecule type: mRNA
A:Residues: 1-461 <TAD>
A:Cross-references: GB:D10445; NID:q220385; PIDN:BAA01235.1; PID:q220386
A:Experimental source: liver.
C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that
s.
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglu
F:1-33/Domain: signal sequence #status predicted <SIG>
F:32-85/Domain: Gla domain homology <GUA>
F:33-41/Domain: propeptide #status predicted <PRO>
F:42-196,199-461/Product: protein C #status predicted <PC>
F:91-130/Domain: EGF homology <EG1>
F:139-174/Domain: EGF homology <EG2>
F:199-461/Domain: heavy chain #status predicted <PC>
F:199-211/Domain: activation peptide #status predicted <ACT>
F:212-461/Product: vitamin K-dependent serine proteinase #status predicted <VIR>
F:213-445/Domain: trypsin homology <TR>
F:47-48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #stat
F:112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F:121-130,139-150,146-159,161-174,182-319,238-254,373-387,398-426/Disulfide bonds: #s
F:215,290,355/Binding site: carboxydrate (Asn) (covalent) #status predicted
F:253,299,402/Active site: His, Asp, Ser #status predicted

```

```

Query Match      35.2%; Score 769; DB 1; Length 461;
Best Local Similarity 36.9%; Pred. No. 6.8e-50;
Matches 159; Conservative 80; Mismatches 150; Indels 42; Gaps 12;

```

```

Qy      1 ANAFLLXLRPGSLKRXCKXKXCSFXAXRIFKDXARTLFWISYSDGQCS----- 52
        ||:|||||
Db      42 ANSFLLEKRPASLEKRECEIEICDFEAEQEIIONVEDTIAFWIKIFKFDGQCCAPPLDHCD 101
        ||:|||||
Qy      53 SPONGSGCKDQLOSYICFLPAFEGRNCEHKKDDQLCVNENGCEQYCDHTGTRKSC 112
        ||:|||||
Db      102 SPCGHGTCIDIGLGGFSQCKGWEGRCCQDEMPQ-LFQDPRVN-NGCLHYCLEESNGRR-C 159
        ||:|||||
Qy      113 RCHGEGSLADGVCSTPVEYPCGKIP-LEKRNASK-----PQRIYGGKCP 160
        ||:|||||
Db      160 ACAPGYELADDDHMKCKSTVNPCCGLGKRWIEKKRILKRDLDLEDELEPDRIVNGTLTX 219
        ||:|||||
Qy      161 KGCPCVOLLVNGAOL-CGGTLINTIWWVSAACFPKIKMRLIAVLGEHDLSEHGD 219
        ||:|||||
Db      220 QGDSFPAAILDSSKKKLACGGVLHTSWVLTAAC---VEETKLTLYRLGTYDLRRDHW 276
        ||:|||||
Qy      220 EQSRRAVQVILPSTYVGLATNHDIALRLRQPPVLTIDHVPFLCLPEMSEBRTLA 278
        ||:|||||

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Db      277  ELDDIDKIKELVHPNTRSSDDNDIALRLAQPATISKTIYPIPLCPNNGLAQJZELLTOAQOE 336
Oy      279  SLVSGMGGLL-----RGATLLEMLVLPPLMTODCLQOESKRVGSDSPNTEYFCAGY 332
Db      337  TVTVMGMOQSDRIKQGRNRRTPI-LTFIPIPIPVARNCEVEVMKNV-----VSENMLCAGI 390
Oy      333  SDGSKDSCKGDGSGPHATHYRGTWTLTGIVSNGOGCATGHHGVYTRVSYOEMLOKLMR 392
Db      391  IGNTRDACCDDGSGPMNVYFPGRTWTLVLGVSMGEGCGHNNNGIITIKVSYLMLHNSYIG 450
Oy      393  SEPRRGVLLRA 403
Db      451  EK---GVSLKS 458

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